



UNITED STATES PATENT AND TRADEMARK OFFICE

S F

UNITED STATES DEPARTMENT OF COMMERCE
United States Patent and Trademark Office
Address: COMMISSIONER FOR PATENTS
P.O. Box 1450
Alexandria, Virginia 22313-1450
www.uspto.gov

| APPLICATION NO. | FILING DATE | FIRST NAMED INVENTOR | ATTORNEY DOCKET NO. | CONFIRMATION NO. |
|---|-------------|----------------------|---------------------|------------------|
| 10/574,333 | 07/21/2008 | Michael Karin | UCSD-10835 | 5879 |
| 7590 | 09/20/2010 | | | |
| Meden & Carroll 101 Howard Street Suite 350 San Francisco, CA 94105 | | | | |
| <p style="text-align: center;">RECEIVED SEP 23 2010 MEDLEN & CARROLL</p> | | | | |
| | | EXAMINER | | |
| | | QIAN, CELINE X | | |
| | | ART UNIT | PAPER NUMBER | |
| | | 1636 | | |
| | | MAIL DATE | DELIVERY MODE | |
| | | 09/20/2010 | PAPER | |

Please find below and/or attached an Office communication concerning this application or proceeding.

The time period for reply, if any, is set in the attached communication.

Seg. Listing due 10/20/10 ed



UNITED STATES PATENT AND TRADEMARK OFFICE

COMMISSIONER FOR PATENTS
UNITED STATES PATENT AND TRADEMARK OFFICE
WASHINGTON, DC 20231
www.uspto.gov

| | | | |
|---|--------------------------|--|-----------------------------------|
| APPLICATION NO./CONTROL NO. 10574333 | FILING DATE 7/21/2008 | FIRST NAMED INVENTOR / PATENT IN REEXAMINATION KARIN ET AL. | ATTORNEY DOCKET NO. UCSD-10835 |
|---|--------------------------|--|-----------------------------------|

| |
|----------------------------|
| EXAMINER CELINE X. QIAN |
|----------------------------|

| | |
|------------------|-------------------|
| ART UNIT 1636 | PAPER 20100916 |
|------------------|-------------------|

DATE MAILED:

Please find below and/or attached an Office communication concerning this application or proceeding.

Commissioner of Patents

This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 C.F.R. § 1.821(a)(1) and (a)(2). However, this application fails to comply with the requirements of 37 C.F.R. §§ 1.821-1.825 for the reason(s) set forth on the attached Notice To Comply With Requirements For Patent Applications Containing Nucleotide Sequence And/Or Amino Acid Sequence Disclosures. Applicant must comply with the requirements of the sequence rules (37 CFR 1.821 - 1.825) before the application can be examined under 35 U.S.C. §§ 131 and 132.

APPLICANT IS GIVEN ONE MONTH FROM THE DATE OF THIS LETTER WITHIN WHICH TO COMPLY WITH THE SEQUENCE RULES, 37 C.F.R.. §§ 1.821-1.825. Failure to comply with these requirements will result in ABANDONMENT of the application under 37 C.F.R. § 1.821(g). Extensions of time may be obtained by filing a petition accompanied by the extension fee under the provisions of 37 C.F.R. § 1.136. In no case may an applicant extend the period for response beyond the six month statutory period. Direct the response to the undersigned. Applicant is requested to return a copy of the attached Notice to Comply with the response.

The addresses below are effective 5 June 2004. Please direct all replies to the United States Patent and Trademark Office via one (1) of the following:

1. Electronically submitted through EFS-Web (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>>, EFS Submission User Manual - ePAVE)
2. Mailed to:

Mail Stop Sequence
Commissioner for Patents
P.O. Box 22313 1450
Alexandria, VA 22313 1450
3. Hand Carry, Federal Express, United Parcel Service or other delivery service to:

U.S. Patent and Trademark Office
Mail Stop Sequence
Customer Window
Randolph Building
401 Dulaney Street
Alexandria, VA 22314

Any inquiry concerning this communication should be directed to Celine Qian at telephone number (571)272-0777. If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Christopher Low, can be reached on 571-272-0951

Celine X Qian
Primary Examiner
Art Unit: 1636

DETAILED ACTION

The communication filed on 7/27/2010 is not fully responsive to the Office communication mailed on 4/27/2010 for the reason(s) set forth on the attached Notice To Comply With The Sequence Rules. The computer readable version of the sequence listing has not been accepted because the description of "n" being amino acid is not acceptable. Applicant must comply with the requirements of the sequence rules (37 CFR 1.821 - 1.825) before the application can be examined under 35 U.S.C. §§ 131 and 132.

Since the reply appears to be bona fide attempt to comply with the requirements of the sequence rules (37 CFR 1.821 - 1.825), applicant is given a TIME PERIOD of **ONE (1) MONTH** from the mailing date of this communication within which to correct the deficiency so as to comply with the sequence rules (37 CFR 1.821 - 1.825) in order to avoid abandonment of the application under 37 CFR 1.821(g). EXTENSIONS OF THIS TIME PERIOD MAY BE GRANTED UNDER 37 CFR 1.136(a).

Any inquiry concerning this communication or earlier communications from the examiner should be directed to CELINE X. QIAN whose telephone number is (571)272-0777. The examiner can normally be reached on 10-6:30 M-F.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Christopher Low can be reached on 571-272-0951. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see <http://pair-direct.uspto.gov>. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free). If you would like assistance from a USPTO Customer Service Representative or access to the automated information system, call 800-786-9199 (IN USA OR CANADA) or 571-272-1000.

/Celine X Qian /
Primary Examiner, Art Unit 1636

| | | |
|-------------------------|------------------------------------|-------------------------------------|
| Notice to Comply | Application No. 10574333 | Applicant(s) KARIN ET AL. |
| | Examiner CELINE X. QIAN | Art Unit 1636 |

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING
NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).
- 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- 7. Other:

Applicant Must Provide:

- An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- An initial or substitute paper copy of the "Sequence Listing", **as well as an amendment specifically directing its entry into the application.**
- A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (571) 272-0731 or (571) 272-0951

For CRF Submission Help, call (571) 272-2510

PatentIn Software Program Support

Technical Assistance. 1-866-217-9197 or 703-305-3028 or 571-272-6845

PatentIn Software is Available At www.USPTO.gov

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR REPLY

| | |
|---|--|
| Celine X Qian Primary Examiner Art Unit: 1636 | |
|---|--|

=====

Sequence Listing could not be accepted.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2010; month=7; day=27; hr=9; min=43; sec=57; ms=320;]

=====

Reviewer Comments:

<210> 57

<211> 10

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_feature

<222> (1)..(1)

<223> n is glycine or alanine.

<220>

<221> misc_feature

<222> (7)..(7)

<223> n is threonine or cysteine.

<220>

<221> misc_feature

<222> (8)..(8)

<223> n is threonine or cysteine.

<400> 57

nggaganntg

10

The above <220>-<223> sections describing the "n's" are errored: "n"
can only represent a single nucleotide; it cannot represent an amino

acid.

<210> 130
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> X can be a or g.

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> X can be t or c.

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> X can be a or g.

<400> 130

Xaa Gly Gly Ala Gly Ala Xaa Thr Thr Xaa
1 5 10

If the above <220>-<223> sections regarding the "Xaa's" are defining them as nucleotides, they are erroneous. If they are denoting amino acids, please spell them out in the <223> responses.

Validated By CRFValidator v 1.0.3

Application No: 10574333 Version No: 1.0

Input Set:

Output Set:

Started: 2010-07-21 14:54:12.726
Finished: 2010-07-21 14:54:16.948
Elapsed: 0 hr(s) 0 min(s) 4 sec(s) 222 ms
Total Warnings: 100
Total Errors: 0
No. of SeqIDs Defined: 134
Actual SeqID Count: 134

| Error code | Error Description |
|------------|---|
| W 213 | Artificial or Unknown found in <213> in SEQ ID (21) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (22) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (23) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (24) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (25) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (26) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (27) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (28) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (29) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (30) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (31) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (32) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (33) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (34) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (35) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (36) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (37) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (38) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (39) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (40) |

Input Set:

Output Set:

Started: 2010-07-21 14:54:12.726
Finished: 2010-07-21 14:54:16.948
Elapsed: 0 hr(s) 0 min(s) 4 sec(s) 222 ms
Total Warnings: 100
Total Errors: 0
No. of SeqIDs Defined: 134
Actual SeqID Count: 134

Error code

Error Description

This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> The Regents of the University of California
Karin, Michael
Bonizzi, Giussepina
Bebien, Mahali

<120> Compositions and Methods for Gene Expression

<130> UCSD-10835

<140> 10574333
<141> 2010-07-21

<150> US 60/508349
<151> 2003-10-01

<150> PCT/US2004/032246
<151> 2004-09-29

<160> 134

<170> PatentIn version 3.5

<210> 1
<211> 700
<212> DNA
<213> Mus musculus

<400> 1
ttcggtaccat ccacccaccc ccagtcgaga gaataggggt acagagggga ggtggcaaaag 60
aaaattcaca atactgagta tctctggag acctgtttgg tctctttgct cggtagcgca 120
gccctacgtt agaatgcata ttcccgggaa tgactgttagt gagactttgg ctggaaatcc 180
aagttattct aactgttagat tggccacgt tgccctaagc ctagcagtcc actgcggcac 240
agacaccctg gacatgaggt gggtcagctt aagttcctgg cacgaaagaa agggtactct 300
ggcaactttt ggatgcggcg aaacagactg tttcgctct caggttctta tttcacggct 360
tgtgccttg acagccccctt agtttctcta tctgcaggat gggagcatta agctctacga 420
cccagcctct ttacaattca ggtccaaaga gcccgc当地 gttggggact gggaaagatca 480
aagggtctcag cacccagcgg agccgc当地 acgtggggcg ccaagaaggg ggtgggtagg 540
tagggactg gaagggcggc tgctccgc当地 gggatgc当地 tcagagaccc cagccacact 600
ccaggccccc cccttgatga gccccgc当地 gccccgc当地 gtttgc当地 ctaaagc当地 660
cagcgctcgc ctccccgtgc cgcactttca ctctcggtcc 700

<210> 2

<211> 10
<212> DNA
<213> Mus musculus

<400> 2
gggagacctg 10

<210> 3
<211> 933
<212> PRT
<213> Homo sapiens

<400> 3

Met Glu Ser Cys Tyr Asn Pro Gly Leu Asp Gly Ile Ile Glu Tyr Asp
1 5 10 15

Asp Phe Lys Leu Asn Ser Ser Ile Val Glu Pro Lys Glu Pro Ala Pro
20 25 30

Glu Thr Ala Asp Gly Pro Tyr Leu Val Ile Val Glu Gln Pro Lys Gln
35 40 45

Arg Gly Phe Arg Phe Arg Tyr Gly Cys Glu Gly Pro Ser His Gly Gly
50 55 60

Leu Pro Gly Ala Ser Ser Glu Lys Gly Arg Lys Thr Tyr Pro Thr Val
65 70 75 80

Lys Ile Cys Asn Tyr Glu Gly Pro Ala Lys Ile Glu Val Asp Leu Val
85 90 95

Thr His Ser Asp Pro Pro Arg Ala His Ala His Ser Leu Val Gly Lys
100 105 110

Gln Cys Ser Glu Leu Gly Ile Cys Ala Val Ser Val Gly Pro Lys Asp
115 120 125

Met Thr Ala Gln Phe Asn Asn Leu Gly Val Leu His Val Thr Lys Lys
130 135 140

Asn Met Met Gly Thr Met Ile Gln Lys Leu Gln Arg Gln Arg Leu Arg
145 150 155 160

Ser Arg Pro Gln Gly Leu Thr Glu Ala Glu Gln Arg Glu Leu Glu Gln
165 170 175

Glu Ala Lys Glu Leu Lys Lys Val Met Asp Leu Ser Ile Val Arg Leu
180 185 190

Arg Phe Ser Ala Phe Leu Arg Ala Ser Asp Gly Ser Phe Ser Leu Pro
195 200 205

Leu Lys Pro Val Thr Ser Gln Pro Ile His Asp Ser Lys Ser Pro Gly
210 215 220

Ala Ser Asn Leu Lys Ile Ser Arg Met Asp Lys Thr Ala Gly Ser Val
225 230 235 240

Arg Gly Gly Asp Glu Val Tyr Leu Leu Cys Asp Lys Val Gln Lys Asp
245 250 255

Asp Ile Glu Val Arg Phe Tyr Glu Asp Asp Glu Asn Gly Trp Gln Ala
260 265 270

Phe Gly Asp Phe Ser Pro Thr Asp Val His Lys Gln Tyr Ala Ile Val
275 280 285

Phe Arg Thr Pro Pro Tyr His Lys Met Lys Ile Glu Arg Pro Val Thr
290 295 300

Val Phe Leu Gln Leu Lys Arg Lys Arg Gly Gly Asp Val Ser Asp Ser
305 310 315 320

Lys Gln Phe Thr Tyr Tyr Pro Leu Val Glu Asp Lys Glu Glu Val Gln
325 330 335

Arg Lys Arg Arg Lys Ala Leu Pro Thr Phe Ser Gln Pro Phe Gly Gly
340 345 350

Gly Ser His Met Gly Gly Ser Gly Gly Ala Ala Gly Gly Tyr Gly
355 360 365

Gly Ala Gly Gly Gly Ser Leu Gly Phe Phe Pro Ser Ser Leu Ala
370 375 380

Tyr Ser Pro Tyr Gln Ser Gly Ala Gly Pro Met Arg Cys Tyr Pro Gly
385 390 395 400

Gly Gly Gly Ala Gln Met Ala Ala Thr Val Pro Ser Arg Asp Ser
405 410 415

Gly Glu Glu Ala Ala Glu Pro Ser Ala Pro Ser Arg Thr Pro Gln Cys
420 425 430

Glu Pro Gln Ala Pro Glu Met Leu Gln Arg Ala Arg Glu Tyr Asn Ala
435 440 445

Arg Leu Phe Gly Leu Ala His Ala Ala Pro Ser Pro Thr Arg Leu Leu
450 455 460

Arg His Arg Gly Arg Arg Ala Leu Leu Ala Gly Gln Arg His Leu Leu
465 470 475 480

Thr Ala Gln Asp Glu Asn Gly Asp Thr Pro Leu His Leu Ala Ile Ile
485 490 495

His Gly Gln Thr Ser Val Ile Glu Gln Ile Val Tyr Val Ile His His
500 505 510

Ala Gln Asp Leu Gly Val Val Asn Leu Thr Asn His Leu His Gln Thr
515 520 525

Pro Leu His Leu Ala Val Ile Thr Gly Gln Thr Ser Val Val Ser Phe
530 535 540

Leu Leu Arg Val Gly Ala Asp Pro Ala Leu Leu Asp Arg His Gly Asp
545 550 555 560

Ser Ala Met His Leu Ala Leu Arg Ala Gly Ala Gly Ala Pro Glu Leu
565 570 575

Leu Arg Ala Leu Leu Gln Ser Gly Ala Pro Ala Val Pro Gln Leu Leu
580 585 590

His Met Pro Asp Phe Glu Gly Leu Tyr Pro Val His Leu Ala Val Arg
595 600 605

Ala Arg Ser Pro Glu Cys Leu Asp Leu Leu Val Asp Ser Gly Ala Glu
610 615 620

Val Glu Ala Thr Glu Arg Gln Gly Gly Arg Thr Ala Leu His Leu Ala
625 630 635 640

Thr Glu Met Glu Glu Leu Gly Leu Val Thr His Leu Val Thr Lys Leu
645 650 655

Arg Ala Asn Val Asn Ala Arg Thr Phe Ala Gly Asn Thr Pro Leu His
660 665 670

Leu Ala Ala Gly Leu Gly Tyr Pro Thr Leu Thr Arg Leu Leu Leu Lys
675 680 685

Ala Gly Ala Asp Ile His Ala Glu Asn Glu Glu Pro Leu Cys Pro Leu
690 695 700

Pro Ser Pro Pro Thr Ser Asp Ser Asp Ser Glu Gly Pro Glu
705 710 715 720

Lys Asp Thr Arg Ser Ser Phe Arg Gly His Thr Pro Leu Asp Leu Thr
725 730 735

Cys Ser Thr Leu Val Lys Thr Leu Leu Leu Asn Ala Ala Gln Asn Thr
740 745 750

Met Glu Pro Pro Leu Thr Pro Pro Ser Pro Ala Gly Pro Gly Leu Ser
755 760 765

Leu Gly Asp Thr Ala Leu Gln Asn Leu Glu Gln Leu Leu Asp Gly Pro
770 775 780

Glu Ala Gln Gly Ser Trp Ala Glu Leu Ala Glu Arg Leu Gly Leu Arg
785 790 795 800

Ser Leu Val Asp Thr Tyr Arg Gln Thr Thr Ser Pro Ser Gly Ser Leu
805 810 815

Leu Arg Ser Tyr Glu Leu Ala Gly Gly Asp Leu Ala Gly Leu Leu Glu
820 825 830

Ala Leu Ser Asp Met Gly Leu Glu Glu Gly Val Arg Leu Leu Arg Gly
835 840 845

Pro Glu Thr Arg Asp Lys Leu Pro Ser Thr Glu Val Lys Glu Asp Ser

| | | | | | | |
|---|-------------|-------------|-------------|-------------|-------------|-----|
| 850 | 855 | 860 | | | | |
| Ala Tyr Gly Ser Gln Ser Val Glu Gln Glu Ala Glu Lys Leu Gly Pro | | | | | | |
| 865 | 870 | 875 | | | | |
| 880 | | | | | | |
| Pro Pro Glu Pro Pro Gly Gly Leu Ser His Gly His Pro Gln Pro Gln | | | | | | |
| 885 | 890 | 895 | | | | |
| Val Thr Asp Leu Leu Pro Ala Pro Ser Pro Leu Pro Gly Pro Pro Val | | | | | | |
| 900 | 905 | 910 | | | | |
| Gln Arg Pro His Leu Phe Gln Ile Leu Phe Asn Thr Pro His Pro Pro | | | | | | |
| 915 | 920 | 925 | | | | |
| Leu Ser Trp Asp Lys | | | | | | |
| 930 | | | | | | |
| <210> 4 | | | | | | |
| <211> 3001 | | | | | | |
| <212> DNA | | | | | | |
| <213> Homo sapiens | | | | | | |
| <400> 4 | | | | | | |
| actttcctgc | cccttccccg | gccaagccca | actccggatc | tcgcctctcca | ccggatctca | 60 |
| cccgccacac | ccggacaggg | ggctggagga | ggcgggcgtc | taaaaattctg | ggaaggcagaa | 120 |
| cctggccgga | gccactagac | agagccgggc | ctagccaga | gacatggaga | gttgctacaa | 180 |
| cccaggctcg | gatggtattta | ttgaatatga | tgatttcaaa | ttgaactcct | ccattgtgga | 240 |
| accgaaggag | ccagccccag | aaacagctga | tggccctac | ctggtgatcg | tggAACAGCC | 300 |
| taagcagaga | ggcttccgat | ttcgatATGG | ctgtgaaggc | ccctccatg | gaggactgcc | 360 |
| cggtgcctcc | agtgagaagg | gccgaaagac | ctatcccact | gtcaagatct | gttaactacga | 420 |
| gggaccagcc | aagatcgagg | tggaccttgt | aacacacagt | gaccCACCTC | gtgtcatgc | 480 |
| ccacagtctg | gtgggcaagc | aatgctcgga | gctggggatc | tgcgcgttt | ctgtggggcc | 540 |
| caaggacatg | actGCCAAT | ttaacaacct | gggtgtcctg | catgtgacta | agaagaacat | 600 |
| gatggggact | atgatacaaa | aacttcagag | gcagcggctc | cgctctaggc | cccaggccct | 660 |
| tacggaggcc | gaggcggccc | agctggagca | agaggccaaa | gaactgaaga | agggtatgga | 720 |
| tctgagttata | gtgcggctgc | gtttctctgc | cttccttaga | gccagtgtatg | gttccttctc | 780 |
| cctgcccctg | aagccagtca | cctcccaagcc | catccatgtat | agcaaatttc | cgggggcattc | 840 |

aaacctgaag atttctcgaa tggacaagac agcaggctct gtgcggggtg gagatgaagt 900
ttatctgctt tgtacaagg tgcaaaaaga tgacatttag gttcggttct atgaggatga 960
tgagaatgga tggcaggcct ttggggactt ctctccaca gatgtgcata aacagtatgc 1020
cattgtgttc cggacacccc cctatcacaa gatgaagatt gagcggcctg taacagtgtt 1080
tctgcaactg aaacgcaagc gaggagggga cgtgtctgat tccaaacagt tcacctatta 1140
ccctctggtg gaagacaagg aagaggtgca gcggaaagcgg aggaaggcct tgcccacett 1200
ctccccagccc ttcgggggtg gctcccacat gggtggaggc tctgggggtg cagccggggg 1260
ctacggagga gctggaggag gtggcagcct cggttttttc ccctccccc tggcctacag 1320
ccccctaccag tccggcgcgg gccccatgcg gtgttaccccg ggaggcgggg gcggggcgc 1380
gatggccgccc acggtgccca gcagggactc cggggagggaa gcccgggagc cgagcgc 1440
ctccaggacc ccccagtgcg agccgcaggc cccggagatg ctgcagcgcag ctgcagagta 1500
caacgcgcgc ctgttcggcc tggcgcacgc agccccgagc cctactcgac tactgcgtca 1560
ccgcggacgc cgccgcgtgc tggcgggaca gcgccacctg ctgacggcgc aggacgagaa 1620
cgagacaca ccactgcacc tagccatcat ccacggcag accagtgtca ttgagcagat 1680
agtctatgtc atccaccacg cccaggacct cggcggtgtc aacccacca accacctgca 1740
ccagacgccc ctgcacctgg cgggtatcac gggcagacg agtgtggtga gctttctgt 1800
gcggtaggt gcagacccag ctctgctgga tcggcatgga gactcagcca tgcatttggc 1860
gctgcggca ggcgcgtgtc ctccctgagct gctgcgtgc ctgcattcaga gtggagctcc 1920
tgctgtgccc cagctgttgc atatgcctga ctttgggggat ctgtatccag tacacctggc 1980
ggtccgagcc cgaaggccctg agtgcctgga tctgctggg gacagtgggg ctgaagtgg 2040
ggccacagag cggcaggggg gacgaacagc cttgcattcta gccacagaga tggaggagct 2100
ggggttggtc acccatctgg tcaccaagct ccggccaaac gtgaacgcgc gcaccccttc 2160
gggaaacaca cccctgcacc tggcagctgg actggggtac ccgaccctca cccgcctct 2220
tctgaaggct ggtgctgaca tccatgctga aaacgaggag cccctgtgcc cactgccttc 2280
accccttacc tctgatagcg actcgagactc tgaaggccct gagaaggaca cccgaagcag 2340
cttccggggc cacacgcctc ttgacccac ttgcagcacc ttgggtgaaga ccttgcgtct 2400
aaatgtgtct cagaacacca tggagccacc cctgaccccg cccagccag cagggccggg 2460
actgtcactt ggtgatacag ctctgcagaa cctggagcag ctgttagacg ggccagaagc 2520
ccagggcagc tggcagagc tggcagagcg tctggggctg cgcagcctgg tagacacgta 2580

| | |
|---|------|
| ccgacagaca acctcaccca gtggcagcct cctgcgcgc tacgagctgg ctggcgaaaa | 2640 |
| cctggcaggt ctactggagg ccctgtctga catgggccta gaggaggag tgaggctgct | 2700 |
| gagggttcca gaaacccgag acaagctgcc cagcacagag gtgaaggaag acagtgcgt | 2760 |
| cgggagccag tcagtggagc aggaggcaga gaagctggc ccacccctg agccaccagg | 2820 |
| agggctctcg caacgggacc cccagcctca ggtgactgac ctgctgcctg cccccagccc | 2880 |
| ccttcccgga cccctgtac aegtccccca cctattcaa atcttattta acacccaca | 2940 |
| cccacccctc agttgggaca aataaaggat tctcatggg aggggaggac cccgaattcc | 3000 |
| t | 3001 |

<210> 5
<211> 899
<212> PRT
<213> Mus musculus

<400> 5

| | | | |
|---|---|----|----|
| Met Asp Asn Cys Tyr Asp Pro Gly Leu Asp Gly Ile Pro Glu Tyr Asp | | | |
| 1 | 5 | 10 | 15 |

| | | |
|---|----|----|
| Asp Phe Glu Phe Ser Pro Ser Ile Val Glu Pro Lys Asp Pro Ala Pro | | |
| 20 | 25 | 30 |

| | | |
|---|----|----|
| Glu Thr Ala Asp Gly Pro Tyr Leu Val Ile Val Glu Gln Pro Lys Gln | | |
| 35 | 40 | 45 |

| | | |
|---|----|----|
| Arg Gly Phe Arg Phe Arg Tyr Gly Cys Glu Gly Pro Ser His Gly Gly | | |
| 50 | 55 | 60 |

| | | | |
|---|----|----|----|
| Leu Pro Gly Ala Ser Ser Glu Lys Gly Arg Lys Thr Tyr Pro Thr Val | | | |
| 65 | 70 | 75 | 80 |

| | | |
|---|----|----|
| Lys Ile Cys Asn Tyr Glu Gly Pro Ala Lys Ile Glu Val Asp Leu Val | | |
| 85 | 90 | 95 |

| | | |
|---|-----|-----|
| Thr His Ser Asp Pro Pro Arg Ala His Ala His Ser Leu Val Gly Lys | | |
| 100 | 105 | 110 |

| | | |
|---|-----|-----|
| Gln Cys Ser Glu Leu Gly Val Cys Ala Val Ser Val Gly Pro Lys Asp | | |
| 115 | 120 | 125 |

Met Thr Ala Gln Phe Asn Asn Leu Gly Val Leu His Val Thr Lys Lys
130 135 140

Asn Met Met Glu Ile Met Ile Gln Lys Leu Gln Arg Gln Arg Leu Arg
145 150 155 160

Ser Lys Pro Gln Gly Leu Thr Glu Ala Glu Arg Arg Glu Leu Glu Gln
165 170 175

Glu Ala Lys Glu Leu Lys Lys Val Met Asp Leu Ser Ile Val Arg Leu
180 185 190

Arg Phe Ser Ala Phe Leu Arg Ala Ser Asp Gly Ser Phe Ser Leu Pro
195 200 205

Leu Lys Pro Val Ile Ser Gln Pro Ile His Asp Ser Lys Ser Pro Gly
210 215 220

Ala Ser Asn Leu Lys Ile Ser Arg Met Asp Lys Thr Ala Gly Ser Val
225 230 235 240

Arg Gly Gly Asp Glu Val Tyr Leu Leu Cys Asp Lys Val Gln Lys Asp
245 250 255

Asp Ile Glu Val Arg Phe Tyr Glu Asp Asp Glu Asn Gly Trp Gln Ala
260 265 270

Phe Gly Asp Phe Ser Pro Thr Asp Val His Lys Gln Tyr Ala Ile Val
275 280 285

Phe Arg Thr Pro Pro Tyr His Lys Met Lys Ile Glu Arg Pro Val Thr
290 295 300

Val Phe Leu Gln Leu Lys Arg Lys Arg Gly Asp Val Ser Asp Ser
305 310 315 320

Lys Gln Phe Thr Tyr Tyr Pro Leu Val Glu Asp Lys Glu Glu Val Gln
325 330 335

Arg Lys Arg Arg Lys Ala Leu Pro Thr Phe Ser Gln Pro Phe Gly Gly
340 345 350

Gly Ser His Met Gly Gly Ser Gly Gly Ser Ala Gly Gly Tyr Gly

355

360

365

Gly Ala Gly Gly Gly Ser Leu Gly Phe Phe Ser Ser Ser Leu Ala
370 375 380

Tyr Asn Pro Tyr Gln Ser Gly Ala Ala Pro Met Gly Cys Tyr Pro Gly
385 390 395 400

Gly Gly Gly Ala Gln Met Ala Gly Ser Arg Arg Asp Thr Asp Ala
405 410 415

Gly Glu Gly Ala Glu Glu Pro Arg Thr Pro Pro Glu Ala Pro Gln Gly
420 425 430

Glu Pro Gln Ala Leu Asp Thr Leu Gln Arg Ala Arg Glu Tyr Asn Ala
435 440 445

Arg Leu Phe Gly Leu Ala Gln Arg Ser Ala Arg Ala Leu Leu Asp Tyr
450 455 460

Gly Val Thr Ala Asp Ala Arg Ala Leu Leu Ala Gly Gln Arg His Leu
465 470 475 480

Leu Met Ala Gln Asp Glu Asn Gly Asp Thr Pro Leu His Leu